

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 02:56:10 ; Search time 1665 Seconds
(without alignments)
16541.650 Million cell updates/sec

Title: US-09-716-536-7
Perfect score: 2007
Sequence: 1 gtgcgtgagcgaatttc.....aaaaaaaaaaaaaaaaaa 2007

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estlum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1075.2	53.6	2696	11	AK012948 Mus muscu
2	1067.2	53.2	1938	11	AK012786 Mus muscu
3	894.4	44.6	959	9	AL560947 AL560947
4	863.4	43.0	887	9	AL560912 AL560912
5	777	38.7	1061	13	BM464844 BM464844
6	685.8	34.2	775	9	AL582241 AL582241

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	MEDLINE	PUBMED	
AK012948	2696 bp	Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810054N23;TRAF-interacting protein, full insert sequence.	AK012948.1	GI:12850018	HTC; CAP trapper.	Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA, clone:2810054N23.	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	99279253	10349636	
AK012948	2696 bp	Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810054N23;TRAF-interacting protein, full insert sequence.	AK012948.1	GI:12850018	HTC; CAP trapper.	Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA, clone:2810054N23.	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20493774	11042159

ALIGNMENTS

ALIGNMENT	Score	Query Match	Length	DB ID	Description
1	1075.2	53.6	2696	11	AK012948 Mus muscu
2	1067.2	53.2	1938	11	AK012786 Mus muscu
3	894.4	44.6	959	9	AL560947 AL560947
4	863.4	43.0	887	9	AL560912 AL560912
5	777	38.7	1061	13	BM464844 BM464844
6	685.8	34.2	775	9	AL582241 AL582241

[illegible]

QY	1495	ACCTTCGTCGTGGTCTGTGAGAACAGTGAAGTCTGACCATATGGCCAGACACATGCTCCACT	1554
Db	1507	ACCTTCCTTAATGTCAG-----TGACCGGTGACCGAGTCAATGTTTGCATTT	1551
QY	1555	TGTAGTCAAGCACTGTCTCAGCAGGAGGTTTGTGACAGAGCCCTACTTTCGGGACCAACC	1614
Db	1552	AGTGGGCAAGACCTGGCTTAACCGGAAGTGTTTTGGAAGATGGGCTCCCTTG-----	1604
QY	1615	TGAGTGTAAAGGGCAGACAAACAGGTGAGGGTGAATGTGACACCCAGAGACTGCTTCC	1674
Db	1605	-----GACCAATGCCAAGAGATGTCCAGAAACACACTTCC	1641
QY	1675	TGCCCTCACCCCTGCCCACTCCTTACAGCTGGAGGTGACATGACCAAGCCCACTGATCTCG	1734
Db	1642	TGTGTTCACATCGCCGCTCCACAC--ACACTGGGAACCAACATGACCAAGTTTAACTGTTCCGA	1699
QY	1735	TCAGAGAGGCTCGC--TCGTGTGCCAGGCTCTGTTTAAAGCCATGATCAGATGGGTGAC	1793
Db	1700	TGCGCAGGGGCTACTTCCACTGATGCCAGGGTTTTGCTATTAAAGCTACAAACCCAGGTGGCTGG	1759
QY	1794	ACTCTTTCTGGGCTCGAGACCAAGGTCATTT	1825
Db	1760	ACTCCTTTTGTTTTATAGAACAGGGTGCACAT	1791

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

PUBMED

REFERENCE

AUTHORS

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TITLE

SECRET

JOURNAL

JOURNAL
OF
MEDICAL
NURSING

RECEIVED
PRINTED

REFERENCES

THE PRESENCE
ALTHOUGH

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

AUTHORS

CCCTTCGTCGGTGCAGAGAACAAGTAGTGCTGACCATTGGCCACACATCCTCGCACT 1554
-----TTAAAGCGGTGACCAAGCATATCTTGGCAATT 1551

CTTAGGCTCAAGACTGCTGCCAGCAGGGCTTTGTGTGACAGAGCCCTACTTTCCGAGCACCC 1614
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CGGCGAAGGCGCTTACTTCCAGTTGCGAGGTTTTGCTTTATAGCTAACACACAGGTGTGGCTGG 1759

CTCTTTCTTG6GCGCTGGAGACCAAGCGTCACTT 1825
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CTCCCTTTTCTTTTATAGAACAAGGTCACT 1791

Ak012786 1938 bp mRNA linear HTC 19-JAN-2002
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810021M06::TRAP-interacting protein, full
insert sequence.

Ak012786
Ak012786.1 GI:12849758
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:2810021M06.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Kono,H., Akiyama,J., Nishi,K., Kitunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamanoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Yoneda,Y., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M.,
Okazaki,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

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2030913
11076861

Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Kono,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanka,I.,
Saito,T., Okazaki,Y., Gajobori,T., Bono,H., Kasukawa,T., Saito,R.,
Sadotchi,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,

OY	806	AGGCGACAGACAGCTACTCTGATTTGGATTTGGATTCAGGCCAAGTTAGACTGAAGTCAGGCCAGA	865
Db	798	AGTTGAAAGACTCTTCACACTGACTGATTCAGGCCAAGTTAGACTGAAGTCAGGCCAGA	857
OY	866	AGGACTTACAGAGTGTCTGACAAAGAAATCATGAGCCTGAAAAAAGAAAGCTAACGATGTGC	925
Db	858	AGGACTTACAAAGTGTCTGACCAAGAGTATTCACAGGCTTAAAGAAAGAAAGCTGATGATCTCC	917
OY	926	AGGAAACCTTGAACCTGTCCACACAGTGGCCAGTGAAGTCTGCACCGCTGTGTTTAGAGA	985
Db	918	AGGGAACCTTGAAGCTGTCCCTCCGGCCAGCAATGAGACGGTCAAGCCGCTGTGTTTGTAGA	977
OY	986	GCCAGGACCCCTGTGGA---GGTGAATCTGAAGTCTCCGGCCGAGCATCTCCGCTGATGTATA	1042
Db	978	GCCAGGACCCCTGTGTGATGATATATACCCCGAGGCTTACCAGCCACTCTTCGGTATGAGA	1037
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Db	1651	TGGGAGACCAATATACCAAGTTTACTGTCTCCGATACAGAGGCTCTACTTCCACTGTGACGG	1710
OY	1762	TCTTGTATTATAGCCATGATGAGATGTGTGACAGCTTCTCTGGGCTGTGAGACACAGCTC	1821
Db	1711	TTTGTCTTATATGACTAACACAGAGTGTGTGTGAGCTCTTGTTTTATTAAGAACAGGCTC	1770
OY	1822	ACTT	1825
Db	1771	ACAT	1774

LOCUS	AL560947	959 bp	mRNA	linear	EST 16-FEB-2001
DEFINITION	AL560947 LTI_NFL010_BC2 Homo sapiens cDNA clone CS0DL005YM09 5				
ACCESSION	AL560947				
VERSION	AL560947.1	GI:12907896			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 959)				
TITLE	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001)				
CONTACT	Contact: Genoscope				
GENOSCOPE	Genoscope - Centre National de Sequencage				
BP	BP 191 91006 EVRY cedex - France				
Email	Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.				
FEATURES	Location/Qualifiers				
Source	1..959				
/organism	"Homo sapiens"				
/db_xref	"taxon:9606"				
/clone	"CS0DL005YM09"				
/clone_lib	"LTI_NFL010_BC2"				
/sex	"male"				
/tissue_type	"B cells from Burkitt lymphoma"				
/note	"vector: pcwvSPORT 6; site:1: NotI; 1st strand cDNA was primed with a NotI-Oligo(gt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcwvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"				
BASE COUNT	259 a 237 c 275 g 185 t 3 others				
ORIGIN					
Query Match	44.6%; Score 894.4; DB 9; Length 959;				
Best Local Similarity	97.1%; Pred. NO. 1.2e-152;				
Matches 927; Conservative	3; Mismatches 23; Indels 2; Gaps 2;				
21	AAGCAAGCGAGGCGGGCGCTCTACGAAGCCGACCTGTACAGTTCTTTGGCTGCT 80				
6	AAGCGAGGCGGGCGGCGCTCTACGAAGCCGACCTGTACAGTTCTTTGGCTGCT 65				
81	GGGCGCTTGATGTCAGAGCATCATGCGTATCGGTCTGTGACATATCGTCCGACTT 140				
66	GGGCGCTTGATGTCAGAGCATCATGCGTATCGGTCTGTGACATATCGTCCGACTT 125				
141	CTTGATCACTCCCGAGAGTGGCGGCATTCATGCGGCCACACCTTCCACTTGCAGTT 200				
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186	CCTAATTCAGTCTTTGAGACAGACACCAAGTGGAGACTGCCACAGTCCCAATCCAGT 245				
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246	TGGCAAAAGAACCATTAATCAATTAACCTCTTTTATCTTGGCCAGAGAGAGAAATGT 305				
321	CTTGATGTCAGATTTCTTAAGATGAATGACATGTCAAGGCCAGCTTTCCAGAA 380				
306	CTTGATGTCAGATTTCTTAAGATGAATGACATGTCAAGGCCAGCTTTCCAGAA 365				
381	AACAAAGGAAG 440				
366	AACAAAGGAAG 425				


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DEFINITION  AGENCOURT_6428661 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5504946
5', mRNA sequence.
ACCESSION   BM464844
VERSION     BM464844.1 GI:18513886
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE   1 (bases 1 to 1061)
            NIH-MGC http://mhc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: c9apbs@remail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L1AM12147 row: b column: 19
            High quality sequence start: 2
            High quality sequence stop: 641.
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                1..1061
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5504946"
                /clone_1ib="NIH_MGC_85"
                /tissue_type="Lymphoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                Average insert size 1.867 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH-MGC Library."
BASE COUNT  282 a 272 c 297 g 202 t 8 others
ORIGIN
Query Match      38.7%; Score 777; DB 13; Length 1061;
Best Local Similarity 97.2%; Pred. No. 2.3e-131;
Matches 808; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

QY 34 CGGGGGCTCTACGAGCGGACCTTAGCAGTTTCTTTGGCTGCTGGCCCTTGAGT 93
    |||||
DB 26 CGGGCGCGTCTACGAGCGGACCTTAGCAGTTTCTTTGGCTGCTGGCCCTTGAGT 85

QY 94 CCAGCATCATGCTATCGCTGCTGTGTGCAATCTGCTCGAGCTTTCTTGATCACTCC 153
    |||||
DB 86 CCAGCATCATGCTATCGCTGCTGTGTGCAATCTGCTCGAGCTTTCTTGATCACTCC 145

QY 154 CGGAGGTGGCCGCAATCCACTGCGGCGCACACCTTCCACTTGGAGTCCATTCAGTCC 213
    |||||
DB 146 CGGAGGTGGCCGCAATCCACTGCGGCGCACACCTTCCACTTGGAGTCCATTCAGTCC 205

QY 214 TTGTGACACAGCACCAGTGGGACCTGCCAGATGCCGAATCCAGGTGGCAAGAAGACC 273
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DB 206 TTGTGACACAGCACCAGTGGGACCTGCCAGATGCCGAATCCAGGTGGCAAGAAGACC 265

QY 274 ATTATCAATTAAGCTTTCTTTGATCTTGGCCAGAGAGAGAGATGCTGGATCCGAGAA 333
    |||||
DB 266 ATTATCAATTAAGCTTTCTTTGATCTTGGCCAGAGAGAGAGATGCTGGATCCGAGAA 325

QY 334 TTCTTAAGAATGAAGTGAAGTGCAGAGCCAGCTTTCCAGAAAGAGAGAGAGAAA 393
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DB 326 TTCTTAAGAATGAAGTGAAGTGCAGAGCCAGCTTTCCAGAAAGAGAGAGAGAAA 385

QY 394 CGAGACAGCAGGTCAATCGACACTTGGCGGATRACGCTGGAAGAGCAATGCTACT 453
    |||||
DB 386 CGAGACAGCAGGTCAATCGACACTTGGCGGATRACGCTGGAAGAGCAATGCTACT 445

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QY 454 GTGATATCTCTGACGAGCGCTTGGCCAGAGCCGAGATGCTGTCCACTGAAGAAAG 513
    |||||
DB 446 GTGATATCTCTGACGAGCGCTTGGCCAGAGCCGAGATGCTGTCCACTGAAGAAAG 505

QY 514 CAGATGAAGTACTTAAAGCAGCAGCAGATGAGACCAACCAACAGAGAGAGCGGCG 573
    |||||
DB 506 CAGATGAAGTACTTAAAGCAGCAGCAGATGAGACCAACCAACAGAGAGAGCGGCG 565

QY 574 CGGCTCAGCAGCAGCAAGTGAAGACATGAGCAGATTTGACTTCTCCAGAGCCAGCTC 633
    |||||
DB 566 CGGCTCAGCAGCAGCAAGTGAAGACATGAGCAGATTTGACTTCTCCAGAGCCAGCTC 625

QY 634 CCTGAGGTGAGAGATGATGATCCGAGACATGGGTGTGGACAGTCCGCGGGAACAGCTG 693
    |||||
DB 626 CCTGAGGTGAGAGATGATGATCCGAGACATGGGTGTGGACAGTCCGCGGGAACAGCTG 685

QY 694 GCTGTACTGTGTCTCTCAAGAAAGATGACAGCAATCTAAAGAGCAGCAGGAGCC 753
    |||||
DB 686 GCTGTACTGTGTCTCTCAAGAAAGATGACAGCAATCTAAAGAGCAGCAGGAGCC 745

QY 754 TCAAGGAGAGTGGCTGACAGCTGAGAGAGATTTGTTTCC-TCCAGAAAGCAAGTTGCA 812
    |||||
DB 746 TCAAGGAGAGTGGCTGACAGCTGAGAGAGATTTGTTTCC-TCCAGAAAGCAAGTTGCA 805

QY 813 GACAGTCTACTCTGAATTTGATCAGGCGCAAG-TTGAAGTGAAGTCAAGCC 862
    |||||
DB 806 GACAGTCTACTCTGAATTTGATCAGGCGCAAG-TTGAAGTGAAGTCAAGCC 856

RESULT 6
AL582241/C 775 bp mRNA linear EST 16-FEB-2001
LOCUS       AL582241 L1L_NFL010_BC2 Homo sapiens cDNA clone CSDDL0051Y108 3
DEFINITION  AL582241 L1L_NFL010_BC2 Homo sapiens cDNA clone CSDDL0051Y108 3
pr ime, mRNA sequence.
ACCESSION   AL582241
VERSION     AL582241.1 GI:12950030
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE   1 (bases 1 to 775)
            Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
            Location/Qualifiers
                1..775
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="CSDDL0051Y108"
                /clone_1ib="L1L_NFL010_BC2"
                /sex="male"
                /tissue_type="B cells from Burkitt lymphoma"
                /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                was primed with a NotI-oligo(dT) primer. Five prime end
                enriched, double-stranded cDNA was digested with Not I and
                cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                vector. Library was normalized. Library was constructed by
                Life Technologies. Contact : Feng Liang Life Technologies,
                a division of Invitrogen 9800 Medical Center Drive
                Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                Email : fliang@lifestech.com URL :
                http://fulllength.invitrogen.com"
BASE COUNT  156 a 199 c 217 g 192 t 11 others
ORIGIN
Query Match      34.2%; Score 685.8; DB 9; Length 775;
Best Local Similarity 95.2%; Pred. No. 9e-115;
Matches 738; Conservative 11; Mismatches 18; Indels 8; Gaps 4;

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OY 1045 GATTCATATGTAACCTTTGATGTGATACTCCCGAGCCCGCCCTCAGACTCCAGCAT 1104
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 775 GATTCATATGTAACCTTTGATGTGATACTCCCGAGCCCGCCCTCAGACTCCAGCAT 716
OY 1105 GGTACTAGAAAAAATTTGGCTTGAAGAGTCACTATCCCAATTAGAGATGCCCAAG 1164
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 715 GGTACTAGAAAAAATTTGGCTTGAAGAGTCACTATCCCAATTAGAGATGCCCAAG 656
OY 1165 AAGATATGCAAGAGCCCGAGAGAGTCCAGACTCTCACTGGGTGGCCAGAGACTGTGA 1224
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 655 AAGATATGCAAGAGCCCGAGAGAGTCCAGACTCTCACTGGGTGGCCAGAGACTGTGA 596
OY 1225 GGAGAGCCAGATGAGAGACTGTTGGTGCCTTCCATATTTTGTCCGGAATGCCATCCTA 1284
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 595 GGAGAGCCAGATGAGAGACTGTTGGTGCCTTCCATATTTTGTCCGGAATGCCATCCTA 536
OY 1285 GGCCAGAAACAGCCCAAGAGCCCGAGAGTCTCTTGGCAGCAAAAGATGTGTAAG 1344
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 535 GGCCAGAAACAGCCCAAGAGCCCGAGAGTCTCTTGGCAGCAAAAGATGTGTAAG 476
OY 1345 ACAGGCTTGATGGGCTGGTGGCGGAGCAAAATTCATCAGGCTTACAGACAGTCATG 1404
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 475 ACAGGCTTGATGGGCTGGTGGCGGAGCAAAATTCATCAGGCTTACAGACAGTCATG 416
OY 1405 ATCCGCCCATTTGCTGTTAAGCCCAAGACAGTTAAGCAGAGGCTGAGGTTGAAGACC 1464
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 415 ATCCGCCCATTTGCTGTTAAGCCCAAGACAGTTAAGCAGAGGCTGAGGTTGAAGACC 356
OY 1465 GTGCTTCTCTCTTCCAGGCGCAAGCTGACACCTTCTGTGCTGAGAACAGTGAATC 1524
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 355 GTGCTTCTCTCTTCCAGGCGCAAGCTGACACCTTCTGTGCTGAGAACAGTGAATC 296
OY 1525 TCACCAATGGCCAGACATGCTGCACTGTGAGTCAAGGACTGTCCAGGAGGG--T 1582
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 295 TCACCAATGGCCAGACATGCTGCACTGTGAGTCAAGGACTGTCCAGGAGGGGTT 236
OY 1583 TTGTGACAGAGACCCCTTACTTTGGGACAGCCTGAGGTGAAGGGCAGCAACAGAGTGA 1642
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 235 TTGTGACAGAGACCCCACTTTGGGACAGCCTGAGGTGAAGGGCAGCAACAGAGTGA 176
OY 1643 GGTGAGTGTGACACCCAGAGACTGCTTCTGCTGCTTCCAGCTTCCAGCTCTTCAAGC 1702
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 175 GGTGAGTGTGACACCCAGAGACTGCTTCAACCTGACCTTCCAGCTTCCAGCTCTTCAAGC 116
OY 1703 TTGAGACTGACAT--GACGAGCCCATGATGCTGTGACAGAGTCTTCTGAGCCTGGA 1757
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 115 TTGAAACTGAAATAGACACRCCCAAMGATCTCTGTGACAGGCTCTCTCTGTATGACACA 56
OY 1758 AGGCTTCTTTATAGC--CATGATCAGATGTGCTGAGACTCTTTCTGGGCTGGA 1811
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 55 GGAGCTCTCTTATAGACCAAGATCAGATGTGTGCTGAGACTCTTTCTGGGCTGGA 1

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RESULT 7
BQ446539/c 777 bp mRNA linear EST 29-MAY-2002
LOCUS BQ446539
DEFINITION UI-H-EU1-azx-9-10-0-UI-s1 NCI CGAP Ctl Homo sapiens cDNA clone
          UI-H-EU1-azx-9-10-0-UI 3', mRNA sequence.
ACCESSION BQ446539
VERSION BQ446539.1 GI:21249651
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 777)
          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
COMMENT JOURNAL Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-tr@mail.nih.gov

```

Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-50, >POLY_A\$Simple_repeat (matched complement)
 Seq primer: M13 FORWARD
 POLY_A=yes.

FEATURES

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source      location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-H-EU1-azx-9-10-0-UI"
/clone_lib="NCI CGAP Ctl"
/tissue_type="Osteoarthritic Cartilage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Knee; Vector: p77T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ctl is a normalized cDNA library containing the
following tissue(s): Osteoarthritic Cartilage The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p77T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCACGCT.
TAG_LIB=UI-H-EU1
TAG_TISSUE=osteothritic cartilage
TAG_SEQ=TAGTACGCT"
BASE COUNT 168 a 208 c 194 g 203 t 4 others
ORIGIN

```

Best Match 33.5% Score 672.6; DB 14; Length 777;
 Query Similarity 96.9% Pred No. 2.2e-112;
 Matches 726; Conservative 0; Mismatches 16; Indels 5; Gaps 4;

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OY 1263 TTTTTCGGAATGCCATCTTCTAGGCGAGAACGCCCAAGAGCCAGTCTGAGTCTTC 1322
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 776 TTTTTCGGAATGCCATCTTCTAGGCGAGAACGCCCAAGAGCCAGTCTGAGTCTTC 717
OY 1323 TTGCAAGAAAGATGTGTGAAGACAGGCTTGCATGTGGCTGCGTGGCCGAGCAAAATTTC 1382
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 716 TTGCAAGAAAGATGTGTGAAGACAGGCTTGCATGTGGCTGCGTGGCCGAGCAAAATTTC 657
OY 1383 CCAGGCTTACTGACACAGTATGATCGGCCCATTTGCTGTTAAGCCCAAGACCAAGTTTA 1442
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 656 CCAGGCTTACTGACACAGTATGATCGGCCCATTTGCTGTTAAGCCCAAGACCAAGTTTA 597
OY 1443 GCAGAGGGTGAAGGGTGAAGACCGTCTTCTCTTCCAGGCCAAGCTGAGACCTTCTCT 1502
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 596 GCAGAGGGTGAAGGGTGAAGACAGTGTCTCTCTTCCAGGCCAAGCTGAGACCTTCTCT 537
OY 1503 GTGGTCTGTAGAAGACAGTGTGTGACCAATGGCCAGACACATGCTTGCACATTTTGAAGTC 1562
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 536 GTGGTCTGTAGAAGACAGTGTGTGACCAATGGCCAGACACATGCTTGCACATTTTGAAGTC 477
OY 1563 AAGGACTGTCCAGGAGAGG--TTTGTGACACAGCCCTTCTTGGGAGCACCTGAGAGT 1620
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 476 AAGGACTGTCCAGGAGAGGTTTGTGTGACACAGCCCACTTTCGGAGCACCTGAGAGT 417
OY 1621 GTAAGGGCAGACAAACAGGTGAAGGTGAGTGTGACACCCAGAGACTGCTTCTCTGAGCCT 1680
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 416 GTAAGGGCAGACAAACAGGTGAAGGTGAGTGTGACACCCAGAGACTGCTTCTCTGAGCCT 357
OY 1681 CACCTGCCCCCACTCTACGACTGGAGGTGACATGACAGCCCACTGATCTGTGACGA 1740
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Db 356 CACCCTGCCCCACTCTACGACTGGAGAGTACATGACCCAGCCCACTGATCTGTGACGA 297
Qy 1741 GGTCTGCT-CTGTGCGAGGCTCTGTTATATAGCATGATGATGCTGACACTT 1799
Db 296 GGTCTGCTCTCTGTGCGAGGCTCTGTTATATAGCATGATGATGCTGACACTT 237
Qy 1800 TCTGGGCTGTGAGACACGCTGCTGTTGACTGCTCTGTGAGCAGAGATGCTTGAGGC 1859
Db 236 TCTGGGCTGTGAGACACGCTGCTGTTGACTGCTCTGTGAGCAGAGATGCTTGAGGC 177
Qy 1860 ATTCAGGACGCTCAGACCCAGCTTCTACCTGCTTGTGACTTCTTA-GCATAGCCT 1918
Db 176 ATTCAGGACGCTCAGACCCAGCTTCTACCTGCTTGTGACTTCTTA-GCATAGCCT 117
Qy 1919 GGGCAGGAGGCTGGGAGATGAGATGATGAGATGATGAGATGAGATGATGAGATGATG 1978
Db 116 GGGCAGGAGGCTGGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGATG 58
Qy 1979 TTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2007
Db 57 TTCATGTAAATAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 29

RESULT 8
BF038722 769 bp mRNA linear EST 20-OCT-2000
LOCUS 601460641F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864082 5',
DEFINITION mRNA sequence.
ACCESSION BF038722 GI:10745770
VERSION BF038722.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 769)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM9605 row: a column: 11
High quality sequence stop: 632.
Location/Qualifiers
1.769
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="NIH_MGC_66"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: ovary; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 184 a 212 c 217 g 156 t
ORIGIN
Query Match 32.9%; Score 659.8; DB 12; Length 769;
Best Local Similarity 97.8%; Pred. No. 4.7e-110;
Matches 701; Conservative 0; Mismatches 12; Indels 4; Gaps 3;
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Qy 930 AACCTGAACCTCCACCACTGAGAGCTGTGAGACCGCTGTTTAAAGAGCCC 989
Db 1 AACCTGAACCTCCACCACTGAGAGCTGTGAGACCGCTGTTTAAAGAGCCC 60
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Qy 990 AGCCCTGTGAGAGTGAATCTGAAGCTCCGCGCCATCTTCCGATGATATGATCT 1049
Db 61 AGCCCTGTGAGAGTGAATCTGAAGCTCCGCGCCATCTTCCGATGATATGATCT 120
Qy 1050 CAATGCTACCTTTGATGTGATATCTCCAGCCGCGCCCTCCAGCTCCAGCATGGTTA 1109
Db 121 CAATGCTACCTTTGATGTGATATCTCCAGCCGCGCCCTCCAGCTCCAGCATGGTTA 180
Qy 1110 CTAGAGAAACCTTGGCTAGAGAGTACACACTCCCAATTCAGATGATGCCCAAGAAGAT 1169
Db 181 CTAGAGAAACCTTGGCTAGAGAGTACACACTCCCAATTCAGATGATGCCCAAGAAGAT 240
Qy 1170 ATCAAGAGCCCGAGAGAGATCCAGCTCTCACTGAGTGGCCAGAGCTGTGAGAGA 1229
Db 241 ATCAAGAGCCCGAGAGAGATCCAGCTCTCACTGAGTGGCCAGAGCTGTGAGAGA 300
Qy 1230 GCCAGATGAGAACTGGTTGGCTCCCTATTTTGTCCGGAATGCCATCTAGGCCA 1289
Db 301 GCCAGATGAGAACTGGTTGGCTCCCTATTTTGTCCGGAATGCCATCTAGGCCA 360
Qy 1290 GAAACAGCCCAAAAGCCCGAGAGTCAAGTCTTGTGAGCAAGATGTGTAAGAGCAGC 1349
Db 361 GAAACAGCCCAAAAGCCCGAGAGTCAAGTCTTGTGAGCAAGATGTGTAAGAGCAGC 420
Qy 1350 CTTCGATGGGCTGGTGGCCGAGCAAAATCATCCAGCTTGTGACAGTCAATGATCCG 1409
Db 421 CTTCGATGGGCTGGTGGCCGAGCAAAATCATCCAGCTTGTGACAGTCAATGATCCG 480
Qy 1410 CCATTCCTCTGTTAAGCCCAAGACCAAGTTAAGCAGAGGAGTGAAGACCTGACC 1469
Db 481 CCATTCCTCTGTTAAGCCCAAGACCAAGTTAAGCAGAGGAGTGAAGACCTGACC 540
Qy 1470 TTCTCTCTCCAGCCCAAGTGTGACACTTCTGTGTCTGTGAGACAGTGTGATCACC 1529
Db 541 TTCTCTCTCCAGCCCAAGTGTGACACTTCTGTGTCTGTGAGACAGTGTGATCACC 600
Qy 1530 AATGGCAGACATGCTCCTCACTTGTAGTGAAGAGCTGTCAGAGCAGG--TTTGTG 1587
Db 601 AATGGCAGACATGCTCCTCAAC-TCATAGCTTAAGAGCTGTCCAGAGGCTTTTGTG 659
Qy 1588 GACAGACCCCTACTTTCGGGAGCAGCCTGAGGTGAAGCAACAAGTGTAGG 1644
Db 660 GACAGACCCCACTTTCGGGAGCAGCCTGAGGTGTAGGAGCAGACAGTGTAGG 715

RESULT 9
BG764118 702 bp mRNA linear EST 15-MAY-2001
LOCUS 602737137F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4862312 5',
DEFINITION mRNA sequence.
ACCESSION BG764118 GI:14074771
VERSION BG764118
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 702)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM1722 row: j column: 09
High quality sequence stop: 697.
Location/Qualifiers
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OY	727	GAGATCTAAAAAGGACGCGAAGGCTTCAGGGAGGTGGCTGACAAAGCTGAGGAAGAT	786
Dd	427	GAGATCTAAAAAGGACGCGAAGGCTTCAGGGAGGTGGCTGACAAAGCTGAGGAAGG-	485
OY	787	TTGTTTTCCTCAGAAAGCAAGTTCGACAGCTCTACTCTGAAATTCGATCAGGCCAAGTTA	846
Dd	486	TTGTTTTCCTCAGAAAGCAAGTTCGACAGCTCTACTCTGAAATTCGATCAGGCCAAGTTA	545
OY	847	GAATCGAAGTACGCCCAAAAGACTTACAGAGTGTGTACAAAGAAATATGAGCTGAAA	906
Dd	546	GAATCGAAGTACGCCCAAAAGACTTACAGAGTGTGTACAAAGAAATATGAGCTGAAA	605
OY	907	AAGAAGCT-AACGATGCTGCAGAGAAACCTT--GAACCTGCCACAGTCGCCAGTGAGACT	963
Dd	606	AAGAAGCTAAACGATGCTGCAGAGAAACCTTGAACCTGTCCACAGCTGGCAGGTAGACT	665
OY	964	GTCGACCCGCTGGTTTATGACAGCCAGCCCGCTGT-GGAGGTGAATCTG--AAGCTCCGC	1020
Dd	666	GTCGACCCGCTGGTTTATGACAGCCAGCCCGCTGTGGAGGTGAATCTGGAATCTCGGC	725
OY	1021	CGGCGATCTT-TCGCTGATGATAT-TGATTCAAAGCTACCTTATATGATGATCTCCG	1078
Dd	726	CGGCGATCTTATCCGCGATGATATGATGATCAATGCTACTTATGATGAGGGTAAATCC	785
OY	1079	CAGCCCGGCGCTTCACGACTCCAGCATGGTTACTACGAAAAACTTTGGCTAGAGAAATC	1138
Dd	786	CAG-CCGCGCGCTCAGCTTCCAGCATGGGTACTAGAAAACCTTGCTGAGAGAGACATCC	844
OY	1139	A 1139	
Dd	845	A 845	

RESULT 11					
LOCUS	BG120736		784 bp	mRNA	linear
DEFINITION	60234738991 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:4442038 5', mRNA sequence.				
ACCESSION	BG120736				
VERSION	BG120736.1	GI:12614245			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Murray-Rot, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 784)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10214 row: b column: 23 High quality sequence stop: 713. Location/Qualifiers 1..784				
FEATURES					
source					

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4442038"
/clone_lib="NIH_MGC_90"
/tissue_type="adenocarcinoma, cell_line"
/lab_host="RDH10B (phage-resistant)"
/notes="Organ: liver; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dt primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

```

BASE COUNT	207 a	200 c	224 g	153 t
ORIGIN				
Query Match	32.4%; Score 651; DB 12; Length 784;			
Best Local Similarity	93.6%; Pred. No. 1.8e-108;			
Matches 735; Conservative	0; Mismatches 40; Indels 10; Gaps 5;			
OY	16	ATTGGAAGCAAGCGGAGGC-----GGGGCGCTCTACGACAGCGGAGCCTGTAGCAGTTTCT	70	
Db	1	ATTGGAACCAAGCGGAGGCGCGGGCGCGCTCTACGAAGGCGCGGACCTGTAGCAGTTTCT	60	
OY	71	TTGGGTGCTGGGGCCCTTGAGTGCAGGCATCATGCCATCCGTCCTGTGACATACT	130	
Db	61	TTGGGTGCTGGGGCCCTTGAGTGCAGGCATCATGCCATCCGTCCTGTGACATACT	120	
OY	131	GCTCCGACTTTTGATGATCTCCGCGACGTCGGCGCATCCAGTCGCGGCGACACCTTCC	190	
Db	121	GCTCCGACTTTTGATGATCTCCGCGACGTCGGCGCATCCAGTCGCGGCGACACCTTCC	180	
OY	191	ACTTGCAGTGCCTTAATTCAGTCTTTGAGACAGCACCAAGTCGGACCTGCCACAGTCC	250	
Db	181	ACTTGCAGTGCCTTAATTCAGTCTTTGAGACAGCACCAAGTCGGACCTGCCACAGTCC	240	
OY	231	GAATCCAGGTTGGCAAAAGAACATTATCATTAAGCTTTCTTTGATTTTCCAGAGAG	310	
Db	241	GAATCCAGGTTGGCAAAAGAACATTATCATTAAGCTTTCTTTGATTTTCCAGAGAG	300	
OY	311	AGGAGAATGTCCTGGATGAGAAATCTTAAAGATGAACCTGACAAATGTCAGAGCCAGC	370	
Db	301	AGGAGAATGTCCTGGATGAGAAATCTTAAAGATGAACCTGACAAATGTCAGAGCCAGC	360	
OY	371	TTTCCACAGAAAGACAAAGAGAAAGACAGACAGCAGTCATCATGCACACTCTGGGGGATA	430	
Db	361	TTTCCACAGAAAGACAAAGAGAAAGACAGACAGCAGTCATCATGCACACTCTGGGGGATA	420	
OY	431	CGCTGGAAGAACGCATCTCTACTGTGTATCTCTGACAGAGCCTTGGGCAAGCCGAGA	490	
Db	421	CGCTGGAAGAACGCATCTCTACTGTGTATCTCTGACAGAGCCTTGGGCAAGCCGAGA	480	
OY	491	TGCTGTGCTCCACATCTGAAAAAGCAGATGAAGTACTTGTAGCAGACGAGGATGAGACCA	550	
Db	481	TGCTGTGCTCCACATCTGAAAAAGCAGATGAAGTACTTGTAGCAGACGAGGATGAGACCA	540	
OY	551	AACAAGCAAGAGAGAGAGCGGGCGGCTCAGAGAGCAAGATGAAGACATGAGAGCAGATTG	610	
Db	541	AACAAGCAAGAGAGAGAGCGGGCGGCTCAGAGAGCAAGATGAAGACATGAGAGCAGATTG	599	
OY	611	AGCTTCTACTCCAGAGCCAGCTCCCTGAGGTGAGAGAGATGATCCGAGACATGGGTGTGG	670	
Db	600	AGCTTCTACTCCAGAGCCAGCTCCCTGAGGTGAGAGAGATGATCCGAGACATGGGTGTGG	659	
OY	671	GACATCTAGCGGTGGAACAGCTGGCTGTGTACTGTGTCTCTCAAGAAAGATACGAGA	730	
Db	660	GACATCTAGCGGTGGAACAGCTGGCTGTGTACTGTGTCTCTCAAGAAAGATACGAGA	717	
OY	731	ATCTTAAAGAGGACAGGAGCCCTCAGGGAGAGTGGCTGACAAAGCTGAGGAAGATTGT	790	
Db	718	ATCTTAAAGAGGACAGGAGCCCTCAGGGAGAGTGGGTGACACCAGAAAGATTGT	775	
OY	791	TTTCC	795	
Db	776	CCTCC	780	
RESULT 12				
B6682548				
LOCUS	B6682548 752 bp mRNA linear EST 01-MAY-2001			
DEFINITION	602624362P1 NCI_GCAP_Skn4 Homo sapiens cDNA clone IMAGE:4749447 5',			
ACCESSION	B6682548			
VERSION	B6682548.1 GI:13913945			
KEYWORDS	EST.			
SOURCE	human			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
ORGANISM	Homo sapiens			
1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
1	(bases 1 to 752)			
NIH-MGC	http://mgi.nci.nih.gov/			
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: cgsab@rmail.nih.gov				
Tissue Procurement: James Cleaver, M.D.				
cDNA Library Preparation: Life Technologies, Inc.				
DNA Sequencing by: Incyte Genomics, Inc.				
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:				
http://image.llnl.gov				
Plate: L10602	row: k	column: 16		
High quality sequence start: 19				
High quality sequence stop: 736				
Location/Qualifiers				
1..752				
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/db_xref="taxon:9606"				
/clone_image="474947"				
/clone_11b="NCL_CGAP_Skn4"				
/tissue_type="squamous cell carcinoma"				
/lab_host="DH10B (TI phage-resistant)"				
/note="Organ: skin; Vector: PCMV-SPOF6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCL_CGAP Library."				
BASE COUNT	200 a	194 c	212 g	146 t
ORIGIN				
Query Match	32.4%	Score 650.2;	DB 12;	Length 752;
Best Local Similarity	97.0%	Pred. No. 2.6e-108;		
Matches 705; Conservative	0;	Mismatches 18;	Indels 4;	Gaps 4
37	GGCGCTACGAGCGGACGCTGTAGCATTCTTTGGCTGCGTGGCCCTTGAGTCCA	96		
11				
22	GGCGCTACGAGCGGACGCTGTAGCATTCTTTGGCTGCGTGGG-CCTTGAGTCCA	80		
97	GGCATTCAGCCATTCGCTCTGTGACATATCTGCTCGACTTCTTGATCAGTCCGC	156		
81	GGCATTCAGCCATTCGCTCTGTGACATATCTGCTCGACTTCTTGATCAGTCCGC	140		
157	GACGTGGCGCCATCCACTGCGGGGCGACACCTTCCACTTGCAGTCCCTAATTCAGTCC	216		
141	GACGTGGCGCCATCCACTGCGGGGCGACACCTTCCACTTGCAGTCCCTAATTCAGTCC	200		
217	GAGACAGCACCAAGTCGACCTGCCACAGTCGCCGATCCAGG-TTGGCGAAAGAACAT	275		
201	GAGACAGCACCAAGTCGACCTGCCACAGTCGCCGATCCAGGTTTGGCGAAAGAACAT	260		
276	TATCATTAAGCTCTTCTTGTGATCTTCCAGAGGAGAGAAATGCTTGATCGAGATT	335		
261	TATCATTAAGCTCTTCTTGTGATCTTCCAGAGGAGAGAAATGCTTGATCGAGATT	320		
336	CTTAAGATGATGAGCAATGTGACAGCCAGCTTCCCGAAGAAAGACAGAGAAAG	395		
321	CTTAAGATGATGAGCAATGTGACAGCCAGCTTCCCGAAGAAAGACAGAGAAAG	380		
396	AGACAGCCAGGATCATCATGACATCTTGGGGGATAGCTGAGAAAGACGATGCTCTGT	455		
381	AGACAGCCAGGATCATCATGACATCTTGGGGGATAGCTGAGAAAGACGATGCTCTGT	440		
456	GGTATCTCTGACAGAGGCTTGGGCGAGGCGAGATGCTGCTCCACACTGAAAAAGCA	515		
441	GGTATCTCTGACAGAGGCTTGGGCGAGGCGAGATGCTGCTCCACACTGAAAAAGCA	500		
516	GATGAAGTACTTAAGAGCAGCAGAGATGAGACCAAGCAAGCAAGAGAGGCGGCGG	575		
501	GATGAAGTACTTAAGAGCAGCAGAGATGAGACCAAGCAAGCAAGAGAGGCGGCGG	560		

QY	576	GCTCAGAGCAAGATGAGACCATGAGCAGATTGAGCTTCTACTCCAGAGCCAGCTCCC	635
Db	561	GCTCAGAGAGCAAGATGAGACCATGAGCAGATTGAGCTTCTACTCCAGAGCCAGAGCC	620
QY	636	TCAGGTGGAGGAGATGATCCCGACATGGGTGTGGACAGCTCAGCGCGTGG -AACAGCTGG	694
Db	621	TCAGGTGGAGGAGATGATCCCGACATGGGTGTGGACAGCGCGTGTGAAACAGTGG	680
QY	695	CTGTCTACTGTTGTCTCT -CAAGAAAGAGTACGAGATCTAAAGAGGACAGGAAGGCC	753
Db	681	CTGTCTACTGTTGTCTCTCTCCCAAGAAAGAGTACGAGATCTAAAGAGGACCGGAAGGCC	740
QY	754	TCAGGCGG 760	
Db	741	TCGCGGG 747	
RESULT 13			
LOCUS	BC420765	908 bp	mRNA
DEFINITION	602448558P1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4586846 5',	linear	EST 14-MAR-2001
ACCESSION	BC420765		
VERSION	BC420765.1	GI:33327271	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 908)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs@email.nih.gov		
	Tissue Procurement: DCID/DTF		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: L1CMI316 row: d column: 15		
	High quality sequence stop: 719.		
FEATURES			
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	/db_xref="taxon:9606"		
	/clone="IMAGE:4586846"		
	/clone_lib="NIH_MGC_14"		
	/tissue_type="renal cell adenocarcinoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: kidney; Vector: pOT7; Site:1: XhoI; Site:2: EcoRI; cDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	235 a 229 c 274 g 170 t		
ORIGIN			
Query Match	31.5%	Score 632.6;	DB 12; Length 908;
Best Local Similarity	89.2%;	Fred. No. 3.9e-105;	
Matches 770; Conservative	0; Mismatches 39;	Indels 54;	Gaps 6;
QY	82	GGCCCTTGAGTCCAGCATCATGCTTACCTGCTGCTGCTGACATATGCTCGACATTC	141
Db	1	GGCCCTTGAGTCCAGCATCATGCTTACCTGCTGCTGCTGACATATGCTCGACATTC	60
QY	142	TTTCGATTCACCTCCCGAGAGTGCCGCCCATTCACCTCGGCCACACCTTCACCTTGGAGTGC	201

